# *Desulfovibrio vulgaris* Hildenborough transcriptomic analysis by Restriction fragment functional display (RFFD)

**M. Santana and J. González**

INRAS-CSIC, 41012 Sevilla, Spain

Sulphate-reducing bacteria reduce sulphate with electrons from carbon substrate thereby producing hydrogen sulphide. This reduction is anaerobic; however the metabolic activity of SRB in oxic zones is frequently higher than in neighbour anoxic zones. The large tolerance to oxygen of SRB is surprising; some are able to respire oxygen in a process coupled to chemiosmotic conservation of energy and ATP production. In the case of *Desulfovibrio vulgaris* Hildenborough sequencing of its genome has confirmed the presence of putative oxygen:oxydoreductase genes. In order to understand why aerobic respiration occurs in *D.vulgaris*, we propose a comparative study of gene expression under aerobic and anaerobic conditions, in wild-type and oxygen:oxidoreductase mutants, focusing on the identification of genes related to the aerobic metabolism. Genes encoding regulators of oxygen response are of special interest. RFFD technique, here described, constitutes a powerful tool to do such study.

**Keywords**: *Desulfovibrio vulgaris*, gene expression, RFFD, oxygen response